SEQUENCE LISTING

<110> JORGE H. CAPDEVILA, MICHAEL WATERMAN, AND VIJAKUMAR HOLLA

<120> COMPOSITIONS AND METHODS RELATING TO
      HYPERTENSION

<130> 22000.0110U2

<150> 60/228,947
<151> 2000-08-29

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 4123
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<221> misc_feature
<222> (1)...(4123)
<223> n = g, a, c or t(u)

<400> 1

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<210> 2
<211> 507
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
     synthetic construct

<400> 2
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Gly Phe Phe Gln Trp Ala Phe Leu Leu Ser Leu Phe Leu Val Leu Phe
            20                  25                  30
Lys Ala Val Gln Phe Tyr Leu Arg Arg Gln Trp Leu Leu Lys Thr Leu
        35                  40                  45
```

Gln His Phe Pro Cys Met Pro Ser His Trp Leu Trp Gly His His Leu
    50   55   60

Lys Asp Lys Glu Leu Gln Gln Ile Leu Ile Trp Val Glu Lys Phe Pro
65   70   75   80

Ser Ala Cys Leu Gln Cys Leu Ser Gly Ser Asn Ile Arg Val Leu Leu
            85   90   95

Tyr Asp Pro Asp Tyr Val Lys Val Val Leu Gly Arg Ser Asp Pro Lys
        100   105   110

Ala Ser Gly Ile Tyr Gln Phe Phe Ala Pro Trp Ile Gly Tyr Gly Leu
        115   120   125

Leu Leu Leu Asn Gly Lys Lys Trp Phe Gln His Arg Arg Met Leu Thr
    130   135   140

Pro Ala Phe His Tyr Asp Ile Leu Lys Pro Tyr Val Lys Ile Met Ala
145   150   155   160

Asp Ser Val Asn Ile Met Leu Asp Lys Trp Glu Lys Leu Asp Gly Gln
            165   170   175

Asp His Pro Leu Glu Ile Phe His Cys Val Ser Leu Met Thr Leu Asp
        180   185   190

Thr Val Met Lys Cys Ala Phe Ser Tyr Gln Gly Ser Val Gln Leu Asp
    195   200   205

Glu Asn Ser Lys Leu Tyr Thr Lys Ala Val Glu Asp Leu Asn Asn Leu
210   215   220

Thr Phe Phe Arg Leu Arg Asn Ala Phe Tyr Lys Tyr Asn Ile Ile Tyr
225   230   235   240

Asn Met Ser Ser Asp Gly Arg Leu Ser His His Ala Cys Gln Ile Ala
            245   250   255

His Glu His Thr Asp Gly Val Ile Lys Met Arg Lys Ser Gln Leu Gln
        260   265   270

Asn Glu Glu Glu Leu Gln Lys Ala Arg Lys Lys Arg His Leu Asp Phe
    275   280   285

Leu Asp Ile Leu Leu Phe Ala Arg Met Glu Asp Arg Asn Ser Leu Ser
    290   295   300

Asp Glu Asp Leu Arg Ala Glu Val Asp Thr Phe Met Phe Glu Gly His
305   310   315   320

Asp Thr Thr Ala Ser Gly Ile Ser Trp Ile Phe Tyr Ala Leu Ala Thr
            325   330   335

His Pro Glu His Gln Gln Arg Cys Arg Glu Glu Val Gln Ser Ile Leu
        340   345   350

Gly Asp Gly Thr Ser Val Thr Trp Asp His Leu Gly Gln Met Pro Tyr
    355   360   365

Thr Thr Met Cys Ile Lys Glu Ala Leu Arg Leu Tyr Pro Pro Val Ile
    370   375   380

Ser Val Ser Arg Glu Leu Ser Ser Pro Val Thr Phe Pro Asp Gly Arg
385   390   395   400

Ser Ile Pro Lys Gly Ile Thr Ala Thr Ile Ser Ile Tyr Gly Leu His
        405   410   415

His Asn Pro Arg Phe Trp Pro Asn Pro Lys Val Phe Asp Pro Ser Arg
    420   425   430

Phe Ala Pro Asp Ser Ser His His Ser His Ala Tyr Leu Pro Phe Ser
    435   440   445

Gly Gly Ser Arg Asn Cys Ile Gly Lys Gln Phe Ala Met Asn Glu Leu
    450   455   460

Lys Val Ala Val Ala Leu Thr Leu Leu Arg Phe Glu Leu Leu Pro Asp
465   470   475   480

Pro Thr Arg Ile Pro Val Pro Ile Ala Arg Leu Val Leu Lys Ser Lys
            485   490   495

Asn Gly Ile His Leu Cys Leu Lys Lys Leu Arg
        500   505

<210> 3
<211> 508
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 3
Met Ser Ala Ser Ala Leu Ser Ser Ile Arg Phe Pro Gly Ser Ile Ser
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Glu Tyr Leu Gln Val Ala Ser Val Leu Ser Leu Leu Leu Leu Leu Phe
            20   25   30
Lys Thr Ala Gln Leu Tyr Leu His Arg Gln Trp Leu Leu Ser Ser Thr
        35   40   45
Gln Gln Phe Pro Ser Pro Pro Ser His Trp Leu Phe Gly His Lys Ile
        50   55   60
Leu Lys Asp Gln Asp Leu Gln Asp Ile Leu Thr Arg Ile Lys Asn Phe
65   70   75   80
Pro Ser Ala Cys Pro Gln Trp Leu Trp Gly Ser Lys Val Arg Ile Gln
                85   90   95
Val Tyr Asp Pro Asp Tyr Met Lys Leu Ile Leu Gly Arg Ser Asp Pro
            100   105   110
Lys Ala Asn Gly Ser Tyr Arg Phe Leu Ala Pro Trp Ile Gly Arg Gly
            115   120   125
Leu Leu Met Leu Asp Gly Gln Thr Trp Phe Gln His Arg Arg Met Leu
        130   135   140
Thr Pro Ala Phe His Tyr Asp Ile Leu Lys Pro Tyr Thr Glu Ile Met
145   150   155   160
Ala Asp Ser Val Arg Val Met Leu Asp Lys Trp Glu Gln Ile Val Gly
                165   170   175
Gln Asp Ser Thr Leu Glu Ile Phe Arg His Ile Thr Leu Met Thr Leu
            180   185   190
Asp Thr Ile Met Lys Cys Ala Phe Ser His Glu Gly Ser Val Gln Leu
            195   200   205
Asp Arg Lys Tyr Lys Ser Tyr Ile Gln Ala Val Glu Asp Leu Asn Asp
        210   215   220
Leu Val Phe Ser Arg Val Arg Asn Ile Phe His Leu Asn Asp Ile Ile
225   230   235   240
Tyr Arg Val Ser Ser Asn Gly Cys Lys Ala Asn Ser Ala Cys Gln Leu
                245   250   255
Ala His Asp His Thr Asp Gln Val Ile Lys Ser Arg Arg Ile Gln Leu
            260   265   270
Gln Asp Glu Glu Glu Leu Glu Lys Leu Lys Lys Lys Arg Arg Leu Asp
            275   280   285
Phe Leu Asp Ile Leu Leu Phe Ala Arg Met Glu Asn Gly Lys Ser Leu
        290   295   300
Ser Asp Lys Asp Leu Arg Ala Glu Val Asp Thr Phe Met Phe Glu Gly
305   310   315   320
His Asp Thr Thr Ala Ser Gly Ile Ser Trp Ile Phe Tyr Ala Leu Ala
                325   330   335
Thr Asn Pro Glu His Gln Gln Arg Cys Arg Lys Glu Ile Gln Ser Leu
            340   345   350
Leu Gly Asp Gly Thr Ser Ile Thr Trp Asn Asp Leu Asp Lys Met Pro
        355   360   365
Tyr Thr Thr Met Cys Ile Lys Glu Ala Leu Arg Ile Tyr Pro Pro Val
    370   375   380

```
Pro Ser Val Ser Arg Glu Leu Ser Ser Pro Val Thr Phe Pro Asp Gly
385                 390                 395                 400
Arg Ser Leu Pro Lys Gly Ile His Val Met Leu Ser Phe Tyr Gly Leu
                405                 410                 415
His His Asn Pro Thr Val Trp Pro Asn Pro Glu Val Phe Asp Pro Ser
            420                 425                 430
Arg Phe Ala Pro Gly Ser Ser Arg His Ser His Ser Phe Leu Pro Phe
        435                 440                 445
Ser Gly Gly Ala Arg Asn Cys Ile Gly Lys Gln Phe Ala Met Asn Glu
    450                 455                 460
Leu Lys Val Ala Val Ala Leu Thr Leu Leu Arg Phe Glu Leu Leu Pro
465                 470                 475                 480
Asp Pro Thr Arg Val Pro Ile Pro Ile Pro Arg Ile Val Leu Lys Ser
            485                 490                 495
Lys Asn Gly Ile His Leu His Leu Lys Glu Leu Gln
            500                 505
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```
<210> 4
<211> 2116
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 4
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caaagaggct gttcaggtcc atcaaccctg gtcttgaaat caagctctgc tcacacccct     180
ctccctcccc caagtaggtg gggcaaccct cctggggttt gcagacagga gggtgttcat     240
tgaaagtgaa ggagagttgg tgatccagaa gctgttgtat catgagtgcc tctgctctga     300
gctccatcag attcccagga agcatctctg agtaccttca agtagcctct gtgctcagcc     360
tgctcctgct gctcttcaag acagcccagc tctacctgca caggcaatgg ctactcagca     420
gtactcagca gttcccatcc ccaccttctc actggctctt tggacacaag atcttaaagg     480
accaggacct tcaagatatt ctaactagga ttaagaattt cccaagtgcc tgtccacagt     540
ggctctgggg aagcaaagtg cgcattcaag tgtatgaccc tgactacatg aagctgattc     600
tggggagatc agacccaaaa gctaatggtt cctacagatt tctagctccc tggattgggc     660
gtggtttgct tatgctggat ggacagacat ggtttcagca ccgacgaatg ttgaccccag     720
ctttccacta tgacattctg aagccttata cggaaatcat ggcagactct gttcgtgtaa     780
tgctggataa atgggaacag attgttggcc aggattccac cctggagatc tttcgacaca     840
tcaccttgat gaccttggac accatcatga agtgtgcctt cagccacgag ggcagtgtcc     900
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tccaataatc ttcacaggac aagacagctc aaatgcatgc tgcctgccat tctgtctttc    1860
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tcttctgaga tccctacttg cttttctctc tacctgtccc taaccagact gcatgtttga    2040
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<210> 5
<211> 519
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 5

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Met Ser Val Ser Val Leu Ser Pro Ser Arg Leu Leu Gly Asp Val Ser
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Gly Ile Leu Gln Ala Ala Ser Leu Leu Ile Leu Leu Leu Leu Leu Ile
            20                  25                  30
Lys Ala Val Gln Leu Tyr Leu His Arg Gln Trp Leu Leu Lys Ala Leu
        35                  40                  45
Gln Gln Phe Pro Cys Pro Pro Ser His Trp Leu Phe Gly His Ile Gln
    50                  55                  60
Glu Leu Gln Gln Asp Gln Glu Leu Gln Arg Ile Gln Lys Trp Val Glu
65                  70                  75                  80
Thr Phe Pro Ser Ala Cys Pro His Trp Leu Trp Gly Gly Lys Val Arg
                85                  90                  95
Val Gln Leu Tyr Asp Pro Asp Tyr Met Lys Val Ile Leu Gly Arg Ser
            100                 105                 110
Asp Pro Lys Ser His Gly Ser Tyr Arg Phe Leu Ala Pro Trp Ile Gly
            115                 120                 125
Tyr Gly Leu Leu Leu Leu Asn Gly Gln Thr Trp Phe Gln His Arg Arg
    130                 135                 140
Met Leu Thr Pro Ala Phe His Tyr Asp Ile Leu Lys Pro Tyr Val Gly
145                 150                 155                 160
Leu Met Ala Asp Ser Val Arg Val Met Leu Asp Lys Trp Glu Glu Leu
                165                 170                 175
Leu Gly Gln Asp Ser Pro Leu Glu Val Phe Gln His Val Ser Leu Met
            180                 185                 190
Thr Leu Asp Thr Ile Met Lys Cys Ala Phe Ser His Gln Gly Ser Ile
            195                 200                 205
Gln Val Asp Arg Asn Ser Gln Ser Tyr Ile Gln Ala Ile Ser Asp Leu
    210                 215                 220
Asn Asn Leu Val Phe Ser Arg Val Arg Asn Ala Phe His Gln Asn Asp
225                 230                 235                 240
Thr Ile Tyr Ser Leu Thr Ser Ala Gly Arg Trp Thr His Arg Ala Cys
                245                 250                 255
Gln Leu Ala His Gln His Thr Asp Gln Val Ile Gln Leu Arg Lys Ala
            260                 265                 270
Gln Leu Gln Lys Glu Gly Glu Leu Glu Lys Ile Lys Arg Lys Arg His
    275                 280                 285
Leu Asp Phe Leu Asp Ile Leu Leu Leu Ala Lys Met Glu Asn Gly Ser
    290                 295                 300
Ile Leu Ser Asp Lys Asp Leu Arg Ala Glu Val Asp Thr Phe Met Phe
305                 310                 315                 320
Glu Gly His Asp Thr Thr Ala Ser Gly Ile Ser Trp Ile Leu Tyr Ala
                325                 330                 335
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Leu Ala Thr His Pro Lys His Gln Glu Arg Cys Arg Glu Glu Ile His
            340                 345                 350
Ser Leu Leu Gly Asp Gly Ala Ser Ile Thr Trp Asn His Leu Asp Gln
            355                 360                 365
Met Pro Tyr Thr Thr Met Cys Ile Lys Glu Ala Leu Arg Leu Tyr Pro
        370                 375                 380
Pro Val Pro Gly Ile Gly Arg Glu Leu Ser Thr Pro Val Thr Phe Pro
385                 390                 395                 400
Asp Gly Arg Ser Leu Pro Lys Gly Ile Met Val Leu Leu Ser Ile Tyr
            405                 410                 415
Gly Leu His His Asn Pro Lys Val Trp Pro Asn Pro Glu Val Phe Asp
            420                 425                 430
Pro Phe Arg Phe Ala Pro Gly Ser Ala Gln His Ser His Ala Phe Leu
            435                 440                 445
Pro Phe Ser Gly Gly Ser Arg Asn Cys Ile Gly Lys Gln Phe Ala Met
        450                 455                 460
Asn Glu Leu Lys Val Ala Thr Ala Leu Thr Leu Leu Arg Phe Glu Leu
465                 470                 475                 480
Leu Pro Asp Pro Thr Arg Ile Pro Ile Pro Ile Ala Arg Leu Val Leu
            485                 490                 495
Lys Ser Lys Asn Gly Ile His Leu Arg Leu Arg Arg Leu Pro Asn Pro
            500                 505                 510
Cys Glu Asp Lys Asp Gln Leu
        515


<210> 6
<211> 2576
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 6
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tgctgatcaa ggcagttcag ctctacctgc acaggcagtg gctgctcaaa gccctccagc     180
agttcccgtg ccctccctcc cactggctct cgggcacat ccaggagctc caacaggacc      240
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tatggggagg caaagttcgt gtccagctct atgaccctga ctatatgaag gtgattctgg     360
ggagatcaga cccgaaatcc atggttcct acagattcct ggctccatgg attgggtacg      420
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cccgtgtgag gaatgccttt caccagaatg acaccatcta cagcctgacc tctgctggcc     780
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gcagagagct cagcactccc gtcaccttcc ctgatgggcg ctccttgccc aaaggtatca    1260
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tgtttgaccc tttccgtttt gcaccgggtt ctgctcaaca cagccacgct ttcctgccct    1380
```

```
tctcaggagg atcaaggaac tgcattggga aacaatttgc catgaacgag ctgaaggtgg    1440
ccacggccct gaccctgctc cgctttgagc tgctgcctga tcccaccagg atccccatcc    1500
ccattgcacg acttgtgttg aaatccaaaa atggaatcca cctgcgtctc aggaggctcc    1560
ctaacccttg tgaagacaag gaccagcttt gagggcctcc acctgccgtc ctgtcttcct    1620
gacccccgct tctgtcccct tcctgtctgc ccatatcctg ttttctgtct gcccaccttc    1680
ccttcttccc acctgcctgc tgtcccccag tctgcctgcc cttctctctc tcacctttct    1740
ccaggctccc tacctgcttg tctacctgtc tcctacccac ctgtatctct tgttgggaga    1800
aaagctgagt gttgggagaa gctgaggccg agcttgcatg tctgacataa tgtaaaagag    1860
tcttgaatca tgtccaggat ccagggtcta aaaccccttg tggcctttgg aacaccaagc    1920
tctgtgctga agggtggaag gctaccctga cgcaccataa tctaagcccg gggcataaaa    1980
cccctcgtgg cttggataga atccagggct cgtggctctg gaatgtgtct ggacttgctg    2040
gctccttgct ccttgctctc ccaggatcaa ttgtatcttg agttaaaaga acctgctctc    2100
cattatctca agtaacagag cagatgctaa accgtcacag ctgtaaattg tgtgcttaat    2160
gcaacatgcc ctttcgaccc acccccatt ctcaccacct gtttctttgt ttgatcacca     2220
ataaataatc tgcacttcca gagctcgggg ccttcacagc ctccatcctt agctttggcg    2280
ccctggaccc actttctctc tcaaactgtc ttttctcact gctttgactc tgccggactt    2340
tgtcacccc acgacctggt gttgggtctg aacaccccaa catccctgaa tctccaccca     2400
cctcccaaac tcctgcctgc cctccagact gtctgcccat acacctgtct ccttcttcct    2460
gcctggcttg tctgttccta tattagtttc ctattactgc tgtaataaac tatcacaatc    2520
tcagtgattt taaataaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaacg gaattc         2576
```

```
<210> 7
<211> 519
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 7
Met Ser Val Ser Val Leu Ser Pro Ser Arg Arg Leu Gly Gly Val Ser
1               5                   10                  15
Gly Ile Leu Gln Val Thr Ser Leu Leu Ile Leu Leu Leu Leu Leu Ile
            20                  25                  30
Lys Ala Ala Gln Leu Tyr Leu His Arg Gln Trp Leu Leu Lys Ala Leu
        35                  40                  45
Gln Gln Phe Pro Cys Pro Ser His Trp Leu Phe Gly His Ile Gln
    50                  55                  60
Glu Phe Gln His Asp Gln Glu Leu Gln Arg Ile Gln Glu Arg Val Lys
65                  70                  75                  80
Thr Phe Pro Ser Ala Cys Pro Tyr Trp Ile Trp Gly Gly Lys Val Arg
                85                  90                  95
Val Gln Leu Tyr Asp Pro Asp Tyr Met Lys Val Ile Leu Gly Arg Ser
            100                 105                 110
Asp Pro Lys Ser His Gly Ser Tyr Arg Phe Leu Ala Pro Arg Ile Gly
        115                 120                 125
Tyr Gly Leu Leu Leu Leu Asn Gly Gln Thr Trp Phe Gln His Arg Arg
    130                 135                 140
Met Leu Thr Pro Ala Phe His Asn Asp Ile Leu Lys Pro Tyr Val Gly
145                 150                 155                 160
Leu Met Ala Asp Ser Val Arg Val Met Leu Asp Lys Trp Glu Glu Leu
                165                 170                 175
Leu Gly Gln Asp Ser Pro Leu Glu Val Phe Gln His Val Ser Leu Met
            180                 185                 190
Thr Leu Asp Thr Ile Met Lys Ser Ala Phe Ser His Gln Gly Ser Ile
        195                 200                 205
Gln Val Asp Arg Asn Ser Gln Ser Tyr Ile Gln Ala Ile Ser Asp Leu
```

```
            210                      215                      220
Asn Ser Leu Val Phe Cys Cys Met Arg Asn Ala Phe His Glu Asn Asp
225                      230                      235                      240
Thr Ile Tyr Ser Leu Thr Ser Ala Gly Arg Trp Thr His Arg Ala Cys
                245                      250                      255
Gln Leu Ala His Gln His Thr Asp Gln Val Ile Gln Leu Arg Lys Ala
                260                      265                      270
Gln Leu Gln Lys Glu Gly Glu Leu Glu Lys Ile Lys Arg Lys Arg His
                275                      280                      285
Leu Asp Phe Leu Asp Ile Leu Leu Leu Ala Lys Met Glu Asn Gly Ser
                290                      295                      300
Ile Leu Ser Asp Lys Asp Leu Arg Ala Glu Val Asp Thr Phe Met Phe
305                      310                      315                      320
Glu Gly His Asp Thr Thr Ala Ser Gly Ile Ser Trp Ile Leu Tyr Ala
                325                      330                      335
Leu Ala Thr His Pro Lys His Gln Glu Arg Cys Arg Glu Glu Ile His
                340                      345                      350
Gly Leu Leu Gly Asp Gly Ala Ser Ile Thr Trp Asn His Leu Asp Gln
                355                      360                      365
Met Pro Tyr Thr Thr Met Cys Ile Lys Glu Ala Leu Arg Leu Tyr Pro
                370                      375                      380
Pro Val Pro Gly Ile Gly Arg Glu Leu Ser Thr Pro Val Thr Phe Pro
385                      390                      395                      400
Asp Gly Arg Ser Leu Pro Lys Gly Ile Met Val Leu Leu Ser Ile Tyr
                405                      410                      415
Gly Leu His His Asn Pro Lys Val Trp Pro Asn Leu Glu Val Phe Asp
                420                      425                      430
Pro Ser Arg Phe Ala Pro Gly Ser Ala Gln His Ser His Ala Phe Leu
                435                      440                      445
Pro Phe Ser Gly Gly Ser Arg Asn Cys Ile Gly Lys Gln Phe Ala Met
                450                      455                      460
Asn Gln Leu Lys Val Ala Arg Ala Leu Thr Leu Leu Arg Phe Glu Leu
465                      470                      475                      480
Leu Pro Asp Pro Thr Arg Ile Pro Ile Pro Ile Ala Arg Leu Val Leu
                485                      490                      495
Lys Ser Lys Asn Gly Ile His Leu Arg Leu Arg Arg Leu Pro Asn Pro
                500                      505                      510
Cys Glu Asp Lys Asp Gln Leu
                515
```

```
<210> 8
<211> 1872
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 8
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aatgctcatt aaatatttgt gaggtacatg gacagggggaa tgtggtagac agctgatgaa      120
gctgttctcc cactgttccc ctaggtggat catccaaagt caatcgattc tgaactctga      180
ggtccaagtt ctgccctccc ccttcactct ccccacaagt gggcgggaca atcctcccat      240
gacttaagca caggtggaca ggggtggtca gagagaggaa ggggcactca gagatccagc      300
aggtgctgca ccatgagtgt ctctgtcctg agccccagca gacgcctggg tggtgtctcc      360
gggatcctcc aagtgacctc cctgctcatt ctgcttctgc tgctgatcaa ggcagctcag      420
ctctacctgc ataggcagtg gctgctcaaa gccctccagc agttcccgtg ccctccctcc      480
```

```
cactggctct tcgggcacat ccaggagttc caacacgacc aggagctaca acggattcag      540
gaacgggtga agacattccc aagtgcctgt ccttattgga tatggggagg caaagttcgt      600
gtccagctct atgaccctga ctatatgaag gtgattctgg ggagatcaga cccgaaatcc      660
catggttcct acagattcct ggctccacgg attgggtacg gcttgctcct gttgaatggg      720
cagacatggt tccagcatcg acggatgctg accccagcct tccacaatga catcctgaag      780
ccatatgtgg ggctcatggc agactctgta cgagtgatgc tggacaaatg ggaagagctc      840
cttggccagg attcccctct ggaggtcttt cagcacgtct ccttgatgac cctggacacc      900
atcatgaaga gtgccttcag ccatcagggc agcatccagg tggacaggaa ttctcagtcc      960
tacatccagg ccattagtga cctgaacagc ctggtttttt gctgtatgag gaatgccttt     1020
catgagaatg acaccatcta cagcctgacc tctgctggcc gctggacaca ccgcgcctgc     1080
cagctggccc atcagcacac agaccaagtg atccaactga ggaaggctca actacagaag     1140
gagggggagc tggagaagat caagaggaag aggcacttgg attttctgga catcctcctc     1200
ttggccaaaa tggagaatgg gagcatcttg tcagacaagg acctccgtgc tgaggtggac     1260
acgttcatgt ttgagggcca cgacaccaca gccagtggga tctcctggat cctctatgct     1320
ctggccacac accccaagca tcaggagagg tgccgggagg agatccatgg cctcctgggt     1380
gatggagcct ccatcacctg gaaccacctg gaccagatgc cctacaccac catgtgcatt     1440
aaggaggcac tgaggctcta cccaccggtg ccaggcattg gaagagagct cagcactccc     1500
gtcaccttcc ctgatgggcg ctccttgccc aaaggtatca tggtcctcct ctccatttat     1560
ggccttcacc acaacccaaa agtgtggccc aacctagagg tgtttgaccc ttcccgtttt     1620
gcaccgggtt ctgctcaaca cagccacgct ttcctgccct tctcaggagg atcaaggaac     1680
tgcatcggga aacaatttgc catgaaccag ctgaaggtgg ccagggccct gaccctgctc     1740
cgctttgagc tgctgcctga tcccaccagg atccccatcc ccattgcacg acttgtgttg     1800
aaatccaaaa atggaatcca cctgcgtctc aggaggctcc ctaacccttg tgaagacaag     1860
gaccagcttt ga                                                         1872
```

<210> 9
<211> 21990
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<221> misc_feature
<222> (1)...(21990)
<223> n = g, a, c or t(u)

<400> 9
```
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn       60
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      120
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      180
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      240
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      300
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      360
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      420
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      480
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      540
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      600
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      660
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      720
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      780
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      840
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      900
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      960
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     1020
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     1080
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     1140
```

```
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1200
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1260
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1320
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1380
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1440
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1500
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1560
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1620
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1680
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1740
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1800
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1860
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    2040
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    2100
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    2160
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    2220
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    2280
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    2340
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    2460
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnggt    2520
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aagccctcca gcagttcccg tgccctccct cccactggct cttcgggcac atccaggagn    2760
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    2820
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    3660
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    4080
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    4560
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    4620
```

```
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    4680
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    5820
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gtctgtaaaa ttccagaaga gagtggctgt tcaaacatca atatctgaaa cctctcccac    6120
gcatccacca agcccaccat gcccaggctg tagtcaaaaa tatttatgaa tactgaatgt    6180
ttaaacaat atgtggggct gaattttcta ttcttttttt ctatttctct attaagaaaa    6240
ttaaattttc tgaaacgtaa attgccccag atctgtaaaa caaatttcat acccacattg    6300
acttgggttc gaagctctaa ttgttgcctg tcctggtcag gaggtgacta ggaaaacatc    6360
aatgtagaaa aacccatggc tctgtattat tcattgtcat tgaagaccta gcctatgtat    6420
ctcaccaatt caccttccta gcccctgggt gttttcctgc tggaacactg agtctgtctt    6480
cctgagccca cattgacctt caggacagaa atagaagtgg atgggagtca agtgggaggt    6540
gacatgggtc aaactgccaa ctgacagaca ccaagaattg atgcagcctc taagactgcc    6600
ttcttagtaa ctcctagttt cctataaagc cctttcttgc ctttcagacc cgaaatccca    6660
tggttcctac agattcctgg ctccatggat tggtatgtgt gcaaactagg actgcagccc    6720
actccctagt caggtttgag ttatttattt ggctcacaga gaacaacaga ttagaggcca    6780
ccactatcat gacctcatcc ccaaatcaag cctcacttcc ttcttctaac aagaccctca    6840
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gttctctcca gacatccttg gcttcacatt tattttacat ctgcccacaa ccctttttcaa    6960
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cagccnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn cctgacacac acacacacac    7200
acacaaacac acattcatgt ctctcttagg gtacggcttg ctcctgttga atgggcagac    7260
atggttccag catcgacgga tgctgacccc agccttccac tatgacatcc tgaagcccta    7320
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnaaccc tgtgtcccac    7440
aggcagacat agacatagac acatggaaca acactctcag gtcattgctg tgagagtaga    7500
gggttcccca gagttgtata aggtaggaga acacccaggc atcaggtcat atccacactt    7560
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      20280
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      20340
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      20400
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      20460
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      20520
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      20580
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      20640
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      20700
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      20760
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      20820
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      20880
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      20940
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      21000
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      21060
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      21120
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      21180
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      21240
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      21300
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      21360
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      21420
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      21480
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      21540
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      21600
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      21660
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      21720
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      21780
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      21840
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      21900
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      21960
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn                                      21990
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